

[illegible]



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FIG. 9a (CONTINUED 1).

CYP3A4, CYP3A5, CYP3A6/7

sites	*	440	*	460	*	480	
HSCYPFLA_CYP3A6/7							-
HSRCYP3_CYP3A7							-
HSP4503A4_CYP3A4							-
S74699_CYP3A5							168
S74700_CYP3A5							477
sites	*	500	*	520	*	540	
HSCYPFLA_CYP3A6/7							-
HSRCYP3_CYP3A7							-
HSP4503A4_CYP3A4							-
S74699_CYP3A5							207
S74700_CYP3A5							391
							537
sites	*	560	*	580	*	600	
HSCYPFLA_CYP3A6/7							-
HSRCYP3_CYP3A7							-
HSP4503A4_CYP3A4							-
S74699_CYP3A5							255
S74700_CYP3A5							450
							597
sites	*	620	*	640	*	660	
HSCYPFLA_CYP3A6/7							-
HSRCYP3_CYP3A7							-
HSP4503A4_CYP3A4							-
S74699_CYP3A5							303
S74700_CYP3A5							508
							656
sites	*	680	*	700	*	720	
HSCYPFLA_CYP3A6/7							-
HSRCYP3_CYP3A7							-
HSP4503A4_CYP3A4							-
S74699_CYP3A5							349
S74700_CYP3A5							568
							716
sites	*	740	*	760	*	780	
HSCYPFLA_CYP3A6/7							-
HSRCYP3_CYP3A7							-
HSP4503A4_CYP3A4							-
S74699_CYP3A5							391
S74700_CYP3A5							628
							776
sites	*	800	*	820	*	840	
HSCYPFLA_CYP3A6/7							-
HSRCYP3_CYP3A7							-
HSP4503A4_CYP3A4							-
S74699_CYP3A5							451
S74700_CYP3A5							688
							836



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FIG. 9a(CONTINUED 2)

CYP3A4, CYP3A5, CYP3A6/7

sites	*	860	*	880	*	900	
HSCYPFLA_CYP3A6/7	-----						-
HSRCYP3_CYP3A7	-----						-
HSP4503A4_CYP3A4	: G T A A G A A T G G T A G G G A A G G G A T C A T G C C T G A T T G C T G G						511
S74699_CYP3A5	: G T A A G T A A T G T G G G G T A G G G T A T C A A G T A A T A T A T G A T G T G						747
S74700_CYP3A5	: G T A A G T A A T G T A G G T A G G G T A T C A A G T A A T A T A T G A T G T G						893
sites	*	920	*	940	*	960	
HSCYPFLA_CYP3A6/7	-----						-
HSRCYP3_CYP3A7	-----						-
HSP4503A4_CYP3A4	: T G G C T A A T T G T T A G G G A A A G G C T G G A A A T T G G T G G T A T G G G A						569
S74699_CYP3A5	: T G G C T A A T T G T T A G G G A A A G G A A G A A A A G G G T G G T G G G G G G						807
S74700_CYP3A5	: T G G C T A A T T G T T A G G G A A A G G A A G A A A A G G G T G G T G G G G G G						950
sites	*	980	*	1000	*	1020	
HSCYPFLA_CYP3A6/7	-----						-
HSRCYP3_CYP3A7	-----						-
HSP4503A4_CYP3A4	: T G G G A A T T G G A T T G A T G A G G G G A T G G A A G T C A A G G G G G G T G G T A A T						629
S74699_CYP3A5	: T A G G A A A T A G G A T G T G T G G G G G A T G G G G G A A G G G G G G T G G T A A T						867
S74700_CYP3A5	: A T A G G A A A T A G G A T G T G T G G G G G A T G G G G G A A G G G G G G T G G T A A T						1010
sites	*	1040	*	1060	*	1080	
HSCYPFLA_CYP3A6/7	-----						-
HSRCYP3_CYP3A7	-----						-
HSP4503A4_CYP3A4	: T G T G T G G G G T T G G T C G G G T A G A T T A G G G A G G - T T G T T G T T G G G T T G						688
S74699_CYP3A5	: T G T G T G A G G G G G T T G G T A G G A A G A T T A T A T G G G G T T G T T G G T G G G T G						927
S74700_CYP3A5	: T G T G T G G G G G G T T G G T A G G A A G A T T A T A T G A G G G - T T G T T G G T G G - G T G						1068
sites	*	1100	*	1120	*	1140	
HSCYPFLA_CYP3A6/7	-----						-
HSRCYP3_CYP3A7	-----						-
HSP4503A4_CYP3A4	: G A G G G T G T G T A G G G T T T T A G G G G G A A G G G A A A T T G G A A A A A A A A						736
S74699_CYP3A5	: A G G G T G T G T A G G G T T T T A G G G G G A A A G T A A A T T A G G A G G G G G T A G A T						987
S74700_CYP3A5	: A G G G T G T G T A G G G T T T T A G G G G G A A A G T A A A T T A G G A G G G G G T A G A T						1128
sites	*	1160	*	1180	*	1200	
HSCYPFLA_CYP3A6/7	-----						-
HSRCYP3_CYP3A7	-----						-
HSP4503A4_CYP3A4	: G G T A G G A T T G T A G G G T G T G G T T G T T G G G A T G A T T T A G T T A T T G G A T G G G A						796
S74699_CYP3A5	: G G T A G G A T T G T A G G G T G T G G T T G T T G G G A T G A T T T A G T A T T T G G A T G G A						1046
S74700_CYP3A5	: - G C T A A G A T T G T A G G G T G T G G T T G T T G G G G A T G G A T T T A G T A T T T G G A T G G A						1187
sites	*	1220	*	1240	*	1260	
HSCYPFLA_CYP3A6/7	-----				CAAT		50
HSRCYP3_CYP3A7	-----						-
HSP4503A4_CYP3A4	: T G A T G G G A A A G G G A G G G A G G G G A T T T A A T G A T T T T T G C C A A T G G T A A						856
S74699_CYP3A5	: T G A T G G A A A A G G G A G G T G A G G G A T A T T T A G G G G T T T T G C - A A T G G T A A						1105
S74700_CYP3A5	: T G A T G G A A A A G G G A G G T G A G G G A T A T T T A G G G G T T T T G C C A A T G G T A A						1247

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FIG. 9(b).

```
A or G
=
MEME repeated motif 9
=====
MEME 'single' motif 9
=====
Yi-consensus
=====
apoE-undefined-site-3
=====
ApoE_B1
=====
APRT-human_US
=====
APRT-CHO_US
=====
1238 AGCTGCAGCCCCACCTCCTTCTCCAGC
TCGACGTCGGGGTGGAGGAAGAGGTCG
```

(B) A

FIG. 9(c).

```
MEME repeated motif 2
=====
MEME repeated motif 2
=====
MEME 'single' motif 9
=====
Yi-consensus
=====
Sp1-TPI_(4)
=====
GCF-consensus
=====
DSE_(1)
=====
IRE_(1)
=====
Sp1_CS4
=====
GC-box_(1)
=====
Sp1-IE-4/5
=====
Sp1-IE-3.3
=====
E2A_CS hsp70.2
=====
E2A_CSSp1-hsp70_(1)
=====
APRT-mouse_US
=====
1379 AGCTGCAGCCCCGCCTCCTTCTCCAGC
TCGACGTCGGGGCGGAGGAAGAGGTCG
```

(B) G



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FIG. 9(d).

```
MEME repeated motif 9
=====
MEME repeated motif 9
=====
MEME repeated motif 3
=====
MEME 'single' motif 6
=====
E-2.7_kb_(3)
=
E1A-F_CS
=====
GH1          MTVGRE_NRS
=====
910 TCTGTCTGGCTGGGCTTGCAAGGATGTGTAG (A) T
    AGACAGACCGACCCGAACGTTCTACACATC
.....
```

FIG. 9(e).

```
MEME repeated motif 9
=====
MEME repeated motif 9
=====
MEME repeated motif 9
=====
MEME repeated motif 3
=====
MEME 'single' motif 6
=====
E-2.7_kb_(3)
=
MBF-I_CS
=====
E1A-F_CS
=====
CNBP-SREMTVGRE_NRS
=====
GH1          MRE_CS2
=====
1052 TCTGTCTGGCTGGGCTTGCAAGGATGTGTAG (A) G
    AGACAGACCGACCGACGTTCTACACATC
.....
```